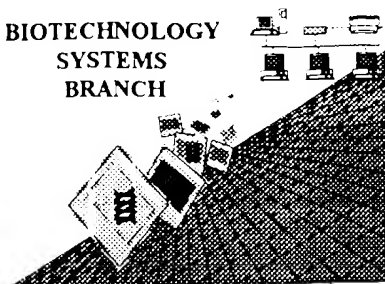


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



1652
JAN 31 2002
TECH CENTER 1600/2900
RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/869,334A
Source: OIP
Date Processed by STIC: 1/17/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE: SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/869,334A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,334A

DATE: 01/17/2002

TIME: 13:44:03

Input Set : A:\ES.txt

Output Set: N:\CRF3\01172002\I869334A.raw

Does Not Comply
Corrected Diskette Needed.

1 <110> APPLICANT: ENDO, Hirofumi YONETANI,
 2 Yashiyuki MIZOGUCHI, Hiroshi HASHIMOTO, Shin-ichi OZAKI,
 W--> 3 <120> TITLE OF INVENTION: Process For Producing HMG-CoA Reductase Inhibitor<130>
 P21289<140>
 W--> 4 <140> CURRENT APPLICATION NUMBER: US/09/869,334A
 W--> 0 <130> FILE REFERENCE:
 C--> 4 <141> CURRENT FILING DATE: 2000-01-28
 W--> 0 <160> NUMBER OF SEQ ID NOS:
 5 <170> SOFTWARE: PatentIn version 3.0<210> 1<211> 396<212> PRT<213> Bacillus

ERRORED SEQUENCES

83 <210> SEQ ID NO: 2<211> 1191<212> DNA<213> Bacillus subtilis<400> 2
 W--> 84 <211> LENGTH:
 W--> 84 <212> TYPE:
 W--> 84 <213> ORGANISM:
 E--> 84 <400> SEQUENCE:
 84 atgaatgtgt taaaccgccc gcaagccttg cagcagcgc tgctcaatgg gaaaaacaaa 60
 86 caggatgcgt atcatcggtt tccatggtat gaatcgatga gaaaggatgc gectgtttcc 120
 88 tttgatgaag aaaaccaagt gtggagcgtt tttctttatg atgatgtcaa aaaagttggt 180
 90 ggggataaag agttgttttc cagttgcatt cgcgcgcaga caagctctat tggaaattcc 240
 92 atcattaaca tggaccgcgc gaagcataca aaaatccgtt cagtcgtgaa caaagccttt 300
 94 actccgcgcg tgatgaagca atgggaaccg agaattcaag aaatcacaga tgaactgatt 360
 96 caaaaatttc agggcgccag tgagtttgac cttgttcacg atttttcata cccgcttccg 420
 98 gttattgtga tatctgagct gctgggagtg ccttcagcgc agatggaaca gtttaaagca 480
 100 tggctctgac tttcgttcag tacaccgaag gataaaagtg aagaagctga aaaagccttt 540
 102 ttggaagaac gagataagtg tgaggaagaa ctggccgcgt tttttgccgg catcatagaa 600
 104 gaaaagcgaa acaaaccgga acaggatatt atttctattt tagtggaagc ggaagaaaca 660
 106 ggcgagaagc tgtccggtga agagctgatt ccgttttgca cgtcgtgct ggtggccgga 720
 108 aatgaaacca ctacaaacct gatttcaaag gcgatgtaca gcatattaga aacgccaggc 780
 110 gtttacgagg aactgcgcag ccatacctgaa ctgatgcctc aggcagtgga ggaagccttg 840
 112 cgtttcagag cgccggccccc ggttttgagg cgcattgccg agcgggatac ggagatcggg 900
 114 gggcacctga ttaaagaagg tgatatggtt ttggcggttg tggcatcggc aaatcgtgat 960
 116 gaagcaaagt ttgacagacc gcacatgttt gatatccgcc gccatcccaa tccgcatatt 1020
 118 gcgtttggcc acggcatcca tttttgcctt gggqccccgc ttgccgtct tgaagcaaatt 1080
 120 atcgcgtaa cgtctttgat ttctgctttt cctcatatgg agtgcgctag tatcactccg 1140
 122 attgaaaaca gtgtgatata cggattaaag agcttccgtg tgaatatgta a 1191
 377 <210> SEQ ID NO: 41<211> 1204<212> DNA<213> Bacillus subtilis<400> 41
 W--> 378 <211> LENGTH:
 W--> 378 <212> TYPE:
 W--> 378 <213> ORGANISM:
 E--> 378 <400> SEQUENCE:
 378 gtgcacaatg aatgtgttaa accgcccggc agccttgacg cgagcgctgc tcaatgggaa 60

09/869,334A

insert a hard return after each response

SEQUENCE LISTING<110> ENDO, Hirofumi / YONETANI,
Yashiyuki / MIZOGUCHI, Hiroshi / HASHIMOTO, Shin-ichi / OZAKI,
Akio<120> Process For Producing HMG-CoA Reductase Inhibitor<130> P21289<140>
09/869,334<141> 2001-07-26<150> PCT JP00/00472<151> 2000-01-28<160> 45 /
<170> PatentIn version 3.0<210> 1<211> 396<212> PRT<213> Bacillus
subtilis<400> 1
↑ ↑ ↑ ↑ ↑

(sample of submitted file)

major format error - please contact
Robert Wax
at 703-306-4119
or 703-308-4216
for assistance

(see next page for
more errors)

insert hard return

09/869,334A **3**

<210> 3<211> 39<212> DNA<213> Artificial<220><223> Artificial Sequence

<400> 3

tttggatccg aattcaaaaag tgctggcgct gttccgttt

39

insufficient explanation
give source of genetic
material - see item 11
on Encl Summary
Sheet

FSI